

SEQUENCE LISTING

<110> Loughney, Kate

<120> Phosphodiesterase 10

<130> 27866/35308

<140> 09/256,000

<141> 1999-02-23

<150> 60/075,508

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<170> PatentIn Ver. 2.0

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<222> (26)..(1423)

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Ile Gln Ser Val Leu Ala Gln Val Ala Glu Gln Phe Ser Arg Ala Phe	
30 35 40	

aaa atc aat gaa ctg aaa gct gaa gtt gca aat cac ttg gct gtc cta	196
Lys Ile Asn Glu Leu Lys Ala Glu Val Ala Asn His Leu Ala Val Leu	
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gag aaa cgc gtg gaa ttg gaa gga cta aaa gtg gtg gag att gag aaa	244
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tgc aag agt gac att aag aag atg agg gag gag ctg gcg gcc aga agc	292
Cys Lys Ser Asp Ile Lys Lys Met Arg Glu Glu Leu Ala Ala Arg Ser	
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agc agg acc aac tgc ccc tgt aag tac agt ttt ttg gat aac cac aag	340
Ser Arg Thr Asn Cys Pro Cys Lys Tyr Ser Phe Leu Asp Asn His Lys	
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Lys Leu Thr Pro Arg Arg Asp Val Pro Thr Tyr Pro Lys Tyr Leu Leu	

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125										130					135					
ctt	tgg	gag	ccc	aat	gag	atg	ctg	agc	tgc	ctg	gag	cac	atg	tac	cac	484				
Leu	Trp	Glu	Pro	Asn	Glu	Met	Leu	Ser	Cys	Leu	Glu	His	Met	Tyr	His					
140										145					150					
gac	ctc	ggg	ctg	gtc	agg	gac	ttc	agc	atc	aac	cct	gtc	acc	ctc	agg	532				
Asp	Leu	Gly	Leu	Val	Arg	Asp	Phe	Ser	Ile	Asn	Pro	Val	Thr	Leu	Arg					
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agg	tgg	ctg	ttc	tgc	gtc	cac	gac	aac	tac	aga	aac	aac	ccc	ttc	cac	580				
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Asn	Phe	Arg	His	Cys	Phe	Cys	Val	Ala	Gln	Met	Met	Tyr	Ser	Met	Val					
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Trp	Leu	Cys	Ser	Leu	Gln	Glu	Lys	Phe	Ser	Gln	Thr	Asp	Ile	Leu	Ile					
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gac	atc	tca	ccg	ctg	gag	aac	cac	cac	tgc	gcc	gtg	gcc	ttc	cag	atc	820				
Asp	Ile	Ser	Pro	Leu	Glu	Asn	His	His	Cys	Ala	Val	Ala	Phe	Gln	Ile					
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Phe	Lys	Gln	Ile	Arg	Gln	Gly	Met	Ile	Thr	Leu	Ile	Leu	Ala	Thr	Asp					
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gac cgt gag aag tca gaa ggc ctt cct gtg gca ccg ttc atg gac cga 1156
Asp Arg Glu Lys Ser Glu Gly Leu Pro Val Ala Pro Phe Met Asp Arg
365 370 375

gac aaa gtg acc aag gcc aca gcc cag att ggg ttc atc aag ttt gtc 1204
Asp Lys Val Thr Lys Ala Thr Ala Gln Ile Gly Phe Ile Lys Phe Val
380 385 390

ctg atc cca atg ttt gaa aca gtg acc aag ctc ttc ccc atg gtt gag 1252
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395 400 405

gag atc atg ctg cag cca ctt tgg gaa tcc cga gat cgc tac gag gag 1300
Glu Ile Met Leu Gln Pro Leu Trp Glu Ser Arg Asp Arg Tyr Glu Glu
410 415 420 425

ctg aag cgg ata gat gac gcc atg aaa gag tta cag aag aag act gac 1348
Leu Lys Arg Ile Asp Asp Ala Met Lys Glu Leu Gln Lys Lys Thr Asp
430 435 440

agc ttg acg tct ggg gcc acc gag aag tcc aga ggg aga agc aga gat 1396
Ser Leu Thr Ser Gly Ala Thr Glu Lys Ser Arg Gly Arg Ser Arg Asp
445 450 455

gtg aaa aac agt gaa gga gac tgt gcc tgaggaaagc ggggggcgtg 1443
Val Lys Asn Ser Glu Gly Asp Cys Ala
460 465

gctgcagttc tggacgggct ggccgagctg cgcgggatcc ttgtgcaggg aagagctgcc 1503

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 <212> PRT
 <213> Homo sapiens

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 Val Ala Glu Gln Phe Ser Arg Ala Phe Lys Ile Asn Glu Leu Lys Ala
 35 40 45
 Glu Val Ala Asn His Leu Ala Val Leu Glu Lys Arg Val Glu Leu Glu
 50 55 60
 Gly Leu Lys Val Val Glu Ile Glu Lys Cys Lys Ser Asp Ile Lys Lys
 65 70 75 80

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Lys	Tyr	Ser	Phe	Leu	Asp	Asn	His	Lys	Lys	Leu	Thr	Pro	Arg	Arg	Asp		
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Val	Pro	Thr	Tyr	Pro	Lys	Tyr	Leu	Leu	Ser	Pro	Glu	Thr	Ile	Glu	Ala		
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Val	Ala	Gln	Met	Met	Tyr	Ser	Met	Val	Trp	Leu	Cys	Ser	Leu	Gln	Glu		
		195					200					205					
Lys	Phe	Ser	Gln	Thr	Asp	Ile	Leu	Ile	Leu	Met	Thr	Ala	Ala	Ile	Cys		
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Arg	Thr	Glu	Leu	Ala	Val	Arg	Tyr	Asn	Asp	Ile	Ser	Pro	Leu	Glu	Asn		
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His	His	Cys	Ala	Val	Ala	Phe	Gln	Ile	Leu	Ala	Glu	Pro	Glu	Cys	Asn		
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Glu	His	Met	Thr	Leu	Leu	Lys	Met	Ile	Leu	Ile	Lys	Cys	Cys	Asp	Ile		
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Ser	Asn	Glu	Val	Arg	Pro	Met	Glu	Val	Ala	Glu	Pro	Trp	Val	Asp	Cys		
		340						345					350				
Leu	Leu	Glu	Glu	Tyr	Phe	Met	Gln	Ser	Asp	Arg	Glu	Lys	Ser	Glu	Gly		
	355					360						365					
Leu	Pro	Val	Ala	Pro	Phe	Met	Asp	Arg	Asp	Lys	Val	Thr	Lys	Ala	Thr		
	370					375					380						
Ala	Gln	Ile	Gly	Phe	Ile	Lys	Phe	Val	Leu	Ile	Pro	Met	Phe	Glu	Thr		

385 390 395 400

Val Thr Lys Leu Phe Pro Met Val Glu Glu Ile Met Leu Gln Pro Leu
 405 410 415

Trp Glu Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile Asp Asp Ala
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Cys Ala
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<210> 3
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 accaaggcca cagcccagat tgggttcac aagtttgccc tgatcccaat gtttgaaaca 120
 gtgaccaagn tcttccccat ggttgaggag atcatgctgc agccactttg ggaatcccga 180
 gatcgntacg aggagctgaa gcggnatagat gacgccatga aagag 225

<210> 4
 <211> 158
 <212> DNA
 <213> Homo sapiens

<220>
 <223> Nucleotides at positions 12, 36, 61, and 109 are
 either A, T, G, or C.

<400> 4
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 gnaaccacca ctgcgccgtg gccttcacaga tcttcgcoga gcctgagtggn aacatcttct 120
 ccaacatccc acctgatggg ttcaagcaga tccgacag 158

<210> 5
 <211> 98
 <212> DNA
 <213> Homo sapiens

<220>

<223> Nucleotides at positions 14, 22, and 50 are either
A, T, C, or G.

<400> 5

gagaacacca ctgngccgtg gncttccaga tctctgccga gcctgagtgn aacatcttct 60
ccaacatccc acctgatggg ttcaagcaga tccgacag 98

<210> 6

<211> 418

<212> DNA

<213> Homo sapiens

<220>

<223> Nucleotides at positions 1, 267, 352, 400, and 411
are either A, T, G, or C.

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gtctctaattg tcaactgtctg ctgcattccc tgcagagcga ccgtgagaag tcagaaggcc 120
ttcccgtagg cccgttcatg gaccgagaca aagtgaccaa ggccacagcc caggattggg 180
tttcatcaag tttgtcctga tcccaatgtt tgaaacagtg accaagctct tcccatggg 240
ttgaggagaga ttcatgctgg cagccanttt ggggaatccc gaggattcgc tacgaggag 300
cttgaagcgg gattagatg gacggccatg gaaaggagtt ttacaggaag gnaggatttg 360
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<210> 7

<211> 428

<212> DNA

<213> Homo sapiens

<220>

<223> Nucleotides at positions 1, 82, 92, 130, 347, 390,
and 396 are either A, T, G, or C.

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ggagctcttc cctgcacaag gntcccgccg antcggccag cccgtccaga actgcagcca 120
cgccccccgn tttcctcagg cacagtctcc ttcactgttt ttcacatctc tgcttctctc 180
tctggacttc tcggtggccc cagacgtcaa gctgtcagtc ttcttctgta actctttcat 240
gggcgtcatc tatccgcttc agctcctcgt aggcgatctc ggggattccc aaagtgggct 300
gcagcatgat cttcctcaac catggggggg aggagcttgg ggcactngtt ttcaaaaatt 360
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100404600T

aatttttg 428

<210> 8
<211> 438
<212> DNA
<213> Homo sapiens

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gtncagggtg cccaggggagc tcttcctgc acaagganc cgcgcantcg gccagcccg 120
ccagaactgc agccacgccc cccgttttcc tcaggcacag tctccttcac tgtttttcac 180
atctctgntt ctctctctgg gantntctgg tgggcccag aacgtcaagc tgtcagtntt 240
cttctgtaac tntttcatgg gcgtcatcta tccgtttcag cttcctcgta ggcgatnttg 300
gggattccca aagtgggctg gcagcatgga tcttcctcaa accatggggg gaaggagttt 360
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<210> 9
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<212> DNA
<213> Mus musculus

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ttactggaag aatattttat gcagagtgc cgtgagaagt ccgaagcctt cctgtggccc 180
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tcctgatccc aatgtttgaa ac 262

<210> 10
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<212> DNA
<213> Mus musculus

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<220>
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                                   Ala Leu Glu
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cac atg tac cac gac ctc ggg ctg gtc agg gac ttc agc atc aac cct 163
His Met Tyr His Asp Leu Gly Leu Val Arg Asp Phe Ser Ile Asn Pro
 5 10 15

gtc acc ctc agg agg tgg ctg ttc tgc gtc cac gac aac tac aga aac 211
Val Thr Leu Arg Arg Trp Leu Phe Cys Val His Asp Asn Tyr Arg Asn
20 25 30 35

aac ccc ttc cac aac ttc cgg cac tgc ttc tgc gtg gcc cag atg atg 259
 Asn Pro Phe His Asn Phe Arg His Cys Phe Cys Val Ala Gln Met Met
 40 45 50

tac agc atg gtc tgg ctc tgc agt ctc cag gag aag ttc tca caa acg 307
Tyr Ser Met Val Trp Leu Cys Ser Leu Gln Glu Lys Phe Ser Gln Thr
55 60 65

gat atc ctg atc cta atg aca gcg gcc atc tgc cac gat ctg gac cat 355
Asp Ile Leu Ile Leu Met Thr Ala Ala Ile Cys His Asp Leu Asp His

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120					125					130						
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135					140					145						
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165					170					175						
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180					185					190					195	
cca Pro	atg Met	gaa Glu	gtc Val	gca Ala	gag Glu	cct Pro	tgg Trp	gtg Val	gac Asp	tgt Cys	tta Leu	tta Leu	gag Glu	gaa Glu	tat Tyr	739
200					205					210						
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215					220					225						
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230					235					240						
atc Ile	aag Lys	ttt Phe	gtc Val	ctg Leu	atc Ile	cca Pro	atg Met	ttt Phe	gaa Glu	aca Thr	gtg Val	acc Thr	aag Lys	ctc Leu	ttc Phe	883
245					250					255						
ccc Pro	atg Met	gtt Val	gag Glu	gag Glu	atc Ile	atg Met	ctg Leu	cag Gln	cca Pro	ctt Leu	tgg Trp	gaa Glu	tcc Ser	cga Arg	gat Asp	931
260					265					270					275	
cgc Arg	tac Tyr	gag Glu	gag Glu	ctg Leu	aag Lys	cgg Arg	ata Ile	gat Asp	gac Asp	gcc Ala	atg Met	aaa Lys	gag Glu	tta Leu	cag Gln	979
280					285					290						
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295					300					305						

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 310 315 320

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 aagagctgcc ctgggcacct ggcaccacaa gaccatgttt tctaagaacc attttgttca 1196
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 35 40 45
 Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser Leu Gln Glu Lys Phe
 50 55 60
 Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala Ala Ile Cys His Asp
 65 70 75 80
 Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln Ile Asn Ala Arg Thr
 85 90 95
 Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro Leu Glu Asn His His
 100 105 110
 Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro Glu Cys Asn Ile Phe
 115 120 125
 Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile Arg Gln Gly Met Ile
 130 135 140
 Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His Ala Glu Ile Met Asp
 145 150 155 160
 Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr Ser Asn Glu Glu His
 165 170 175
 Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys Cys Asp Ile Ser Asn
 180 185 190
 Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp Val Asp Cys Leu Leu
 195 200 205

Glu Glu Tyr Phe Met Gln Ser Asp Arg Glu Lys Ser Glu Gly Leu Pro
 210 215 220
 Val Ala Pro Phe Met Asp Arg Asp Lys Val Thr Lys Ala Thr Ala Gln
 225 230 235 240
 Ile Gly Phe Ile Lys Phe Val Leu Ile Pro Met Phe Glu Thr Val Thr
 245 250 255
 Lys Leu Phe Pro Met Val Glu Glu Ile Met Leu Gln Pro Leu Trp Glu
 260 265 270
 Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile Asp Asp Ala Met Lys
 275 280 285
 Glu Leu Gln Lys Lys Thr Asp Ser Leu Thr Ser Gly Ala Thr Glu Lys
 290 295 300
 Ser Arg Glu Arg Ser Arg Asp Val Lys Asn Ser Glu Gly Asp Cys Ala
 305 310 315 320

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 <213> Homo sapiens

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 Met Gly Ser Gly Ser Ser Tyr Arg Pro Lys Ala
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 atc tac ctg gac atc gat gga cgc att cag aag gta atc ttc agc aag 157
 Ile Tyr Leu Asp Ile Asp Gly Arg Ile Gln Lys Val Ile Phe Ser Lys
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 tac tgc aac tcc agc gac atc atg gac ctg ttc tgc atc gcc acc ggc 205
 Tyr Cys Asn Ser Ser Asp Ile Met Asp Leu Phe Cys Ile Ala Thr Gly
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 ctg cct cgg aac acg acc atc tcc ctg ctg acc acc gac gac gcc atg 253
 Leu Pro Arg Asn Thr Thr Ile Ser Leu Leu Thr Thr Asp Asp Ala Met
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 gtc tcc atc gac ccc acc atg ccc gcg aat tca gaa cgc act ccg tac 301
 Val Ser Ile Asp Pro Thr Met Pro Ala Asn Ser Glu Arg Thr Pro Tyr
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 aaa gtg aga cct gtg gcc atc aag caa ctc tcc gag aga gaa gaa tta 349
 Lys Val Arg Pro Val Ala Ile Lys Gln Leu Ser Glu Arg Glu Glu Leu
 80 85 90

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Ile Gln Ser Val Leu Ala Gln Val Ala Glu Gln Phe Ser Arg Ala Phe	
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aaa atc aat gaa ctg aaa gct gaa gtt gca aat cac ttg gct gtc cta	445
Lys Ile Asn Glu Leu Lys Ala Glu Val Ala Asn His Leu Ala Val Leu	
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gag aaa cgc gtg gaa ttg gaa gga cta aaa gtg gtg gag att gag aaa	493
Glu Lys Arg Val Glu Leu Glu Gly Leu Lys Val Val Glu Ile Glu Lys	
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Cys Lys Ser Asp Ile Lys Lys Met Arg Glu Glu Leu Ala Ala Arg Ser	
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agc agg acc aac tgc ccc tgt aag tac agt ttt ttg gat aac cac aag	589
Ser Arg Thr Asn Cys Pro Cys Lys Tyr Ser Phe Leu Asp Asn His Lys	
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Lys Leu Thr Pro Arg Arg Asp Val Pro Thr Tyr Pro Lys Tyr Leu Leu	
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tct cca gag acc atc gag gcc ctg cgg aag ccg acc ttt gac gtc tgg	685
Ser Pro Glu Thr Ile Glu Ala Leu Arg Lys Pro Thr Phe Asp Val Trp	
190 195 200	
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Leu Trp Glu Pro Asn Glu Met Leu Ser Cys Leu Glu His Met Tyr His	
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Asp Leu Gly Leu Val Arg Asp Phe Ser Ile Asn Pro Val Thr Leu Arg	
225 230 235	
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Arg Trp Leu Phe Cys Val His Asp Asn Tyr Arg Asn Asn Pro Phe His	
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Asn Phe Arg His Cys Phe Cys Val Ala Gln Met Met Tyr Ser Met Val	
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Trp Leu Cys Ser Leu Gln Glu Lys Phe Ser Gln Thr Asp Ile Leu Ile	
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cta atg aca gcg gcc atc tgc cac gat ctg gac cat ccc ggc tac aac	973
Leu Met Thr Ala Ala Ile Cys His Asp Leu Asp His Pro Gly Tyr Asn	
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Asn Thr Tyr Gln Ile Asn Ala Arg Thr Glu Leu Ala Val Arg Tyr Asn	
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ctc gcc gag cct gag tgc aac atc ttc tcc aac atc cca cct gat ggg Leu Ala Glu Pro Glu Cys Asn Ile Phe Ser Asn Ile Pro Pro Asp Gly 335 340 345			1117
ttc aag cag atc cga cag gga atg atc aca tta atc ttg gcc act gac Phe Lys Gln Ile Arg Gln Gly Met Ile Thr Leu Ile Leu Ala Thr Asp 350 355 360			1165
atg gca aga cat gca gaa att atg gat tct ttc aaa gag aaa atg gag Met Ala Arg His Ala Glu Ile Met Asp Ser Phe Lys Glu Lys Met Glu 365 370 375 380			1213
aat ttt gac tac agc aac gag gag cac atg acc ctg ctg aag atg att Asn Phe Asp Tyr Ser Asn Glu Glu His Met Thr Leu Leu Lys Met Ile 385 390 395			1261
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 Thr Thr Ile Ser Leu Leu Thr Thr Asp Asp Ala Met Val Ser Ile Asp
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 Pro Thr Met Pro Ala Asn Ser Glu Arg Thr Pro Tyr Lys Val Arg Pro
 65 70 75 80
 Val Ala Ile Lys Gln Leu Ser Glu Arg Glu Glu Leu Ile Gln Ser Val
 85 90 95
 Leu Ala Gln Val Ala Glu Gln Phe Ser Arg Ala Phe Lys Ile Asn Glu
 100 105 110
 Leu Lys Ala Glu Val Ala Asn His Leu Ala Val Leu Glu Lys Arg Val
 115 120 125
 Glu Leu Glu Gly Leu Lys Val Val Glu Ile Glu Lys Cys Lys Ser Asp
 130 135 140
 Ile Lys Lys Met Arg Glu Glu Leu Ala Ala Arg Ser Ser Arg Thr Asn
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 Cys Pro Cys Lys Tyr Ser Phe Leu Asp Asn His Lys Lys Leu Thr Pro
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 Arg Arg Asp Val Pro Thr Tyr Pro Lys Tyr Leu Leu Ser Pro Glu Thr
 180 185 190
 Ile Glu Ala Leu Arg Lys Pro Thr Phe Asp Val Trp Leu Trp Glu Pro
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 Asn Glu Met Leu Ser Cys Leu Glu His Met Tyr His Asp Leu Gly Leu
 210 215 220
 Val Arg Asp Phe Ser Ile Asn Pro Val Thr Leu Arg Arg Trp Leu Phe
 225 230 235 240
 Cys Val His Asp Asn Tyr Arg Asn Asn Pro Phe His Asn Phe Arg His
 245 250 255

Cys Phe Cys Val Ala Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser
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 Leu Gln Glu Lys Phe Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala
 275 280 285
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 290 295 300
 Ile Asn Ala Arg Thr Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro
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 Leu Glu Asn His His Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro
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 Glu Cys Asn Ile Phe Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile
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 Arg Gln Gly Met Ile Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His
 355 360 365
 Ala Glu Ile Met Asp Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr
 370 375 380
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 385 390 395 400
 Cys Asp Ile Ser Asn Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp
 405 410 415
 Val Asp Cys Leu Leu Glu Glu Tyr Phe Met Gln Ser Asp Arg Glu Lys
 420 425 430
 Ser Glu Gly Leu Pro Val Ala Pro Phe Met Asp Arg Asp Lys Val Thr
 435 440 445
 Lys Ala Thr Ala Gln Ile Gly Phe Ile Lys Phe Val Leu Ile Pro Met
 450 455 460
 Phe Glu Thr Val Thr Lys Leu Phe Pro Met Val Glu Glu Ile Met Leu
 465 470 475 480
 Gln Pro Leu Trp Glu Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile
 485 490 495
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Cys Asn Ser Ser Asp Ile Met Asp Leu Phe Cys Ile Ala Thr Gly Leu
20 25 30

cct cgg aac acg acc atc tcc ctg ctg acc acc gac gac gcc atg gtc 145
Pro Arg Asn Thr Thr Ile Ser Leu Leu Thr Thr Asp Asp Ala Met Val
35 40 45

tcc atc gac ccc acc atg ccc gcg aat tca gaa cgc act ccg tac aaa 193
Ser Ile Asp Pro Thr Met Pro Ala Asn Ser Glu Arg Thr Pro Tyr Lys
50 55 60

gtg aga cct gtg gcc atc aag caa ctc tcc gct gat gtc gag gac aag 241
Val Arg Pro Val Ala Ile Lys Gln Leu Ser Ala Asp Val Glu Asp Lys
65 70 75 80

aga acc aca agc cgt ggc cag tct gct gag aga cca ctg agg gac aga 289
Arg Thr Thr Ser Arg Gly Gln Ser Ala Glu Arg Pro Leu Arg Asp Arg
85 90 95

cgg gtt gtg ggc ctg gag cag ccc cgg agg gaa gga gca ttt gaa agt 337
Arg Val Val Gly Leu Glu Gln Pro Arg Arg Glu Gly Ala Phe Glu Ser
100 105 110

gga cag gta gag ccc agg ccc aga gag ccc cag ggc tgc tac cag gaa 385
Gly Gln Val Glu Pro Arg Pro Arg Glu Pro Gln Gly Cys Tyr Gln Glu
115 120 125

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Gly Gln Arg Ile Pro Pro Glu Arg Glu Glu Leu Ile Gln Ser Val Leu
130 135 140

gcg cag gtt gca gag cag ttc tca aga gca ttc aaa atc aat gaa ctg 481
Ala Gln Val Ala Glu Gln Phe Ser Arg Ala Phe Lys Ile Asn Glu Leu
145 150 155 160

aaa gct gaa gtt gca aat cac ttg gct gtc cta gag aaa cgc gtg gaa 529
Lys Ala Glu Val Ala Asn His Leu Ala Val Leu Glu Lys Arg Val Glu
165 170 175

ttg gaa gga cta aaa gtg gtg gag att gag aaa tgc aag agt gac att 577
Leu Glu Gly Leu Lys Val Val Glu Ile Glu Lys Cys Lys Ser Asp Ile
180 185 190

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Pro Cys Lys Tyr Ser Phe Leu Asp Asn His Lys Lys Leu Thr Pro Arg	
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Arg Asp Val Pro Thr Tyr Pro Lys Tyr Leu Leu Ser Pro Glu Thr Ile	
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gag atg ctg agc tgc ctg gag cac atg tac cac gac ctc ggg ctg gtc	817
Glu Met Leu Ser Cys Leu Glu His Met Tyr His Asp Leu Gly Leu Val	
260 265 270	
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Arg Asp Phe Ser Ile Asn Pro Val Thr Leu Arg Arg Trp Leu Phe Cys	
275 280 285	
gtc cac gac aac tac aga aac aac ccc ttc cac aac ttc cgg cac tgc	913
Val His Asp Asn Tyr Arg Asn Asn Pro Phe His Asn Phe Arg His Cys	
290 295 300	
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Phe Cys Val Ala Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser Leu	
305 310 315 320	
cag gag aag ttc tca caa acg gat atc ctg atc cta atg aca gcg gcc	1009
Gln Glu Lys Phe Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala Ala	
325 330 335	
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Ile Cys His Asp Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln Ile	
340 345 350	
aat gcc cgc aca gag ctg gcg gtc cgc tac aat gac atc tca ccg ctg	1105
Asn Ala Arg Thr Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro Leu	
355 360 365	
gag aac cac cac tgc gcc gtg gcc ttc cag atc ctc gcc gag cct gag	1153
Glu Asn His His Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro Glu	
370 375 380	
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Cys Asn Ile Phe Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile Arg	
385 390 395 400	
cag gga atg atc aca tta atc ttg gcc act gac atg gca aga cat gca	1249
Gln Gly Met Ile Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His Ala	
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gaa att atg gat tct ttc aaa gag aaa atg gag aat ttt gac tac agc	1297
Glu Ile Met Asp Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr Ser	
420 425 430	
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Pro Arg Asn Thr Thr Ile Ser Leu Leu Thr Thr Asp Asp Ala Met Val
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Ser Ile Asp Pro Thr Met Pro Ala Asn Ser Glu Arg Thr Pro Tyr Lys
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Val Arg Pro Val Ala Ile Lys Gln Leu Ser Ala Asp Val Glu Asp Lys
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Arg Thr Thr Ser Arg Gly Gln Ser Ala Glu Arg Pro Leu Arg Asp Arg
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Arg Val Val Gly Leu Glu Gln Pro Arg Arg Glu Gly Ala Phe Glu Ser
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Gly Gln Val Glu Pro Arg Pro Arg Glu Pro Gln Gly Cys Tyr Gln Glu
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Gly Gln Arg Ile Pro Pro Glu Arg Glu Glu Leu Ile Gln Ser Val Leu
130 135 140

Ala Gln Val Ala Glu Gln Phe Ser Arg Ala Phe Lys Ile Asn Glu Leu
145 150 155 160

Lys Ala Glu Val Ala Asn His Leu Ala Val Leu Glu Lys Arg Val Glu
165 170 175

Leu Glu Gly Leu Lys Val Val Glu Ile Glu Lys Cys Lys Ser Asp Ile
180 185 190

Lys Lys Met Arg Glu Glu Leu Ala Ala Arg Ser Ser Arg Thr Asn Cys
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Pro Cys Lys Tyr Ser Phe Leu Asp Asn His Lys Lys Leu Thr Pro Arg
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Arg Asp Val Pro Thr Tyr Pro Lys Tyr Leu Leu Ser Pro Glu Thr Ile
225 230 235 240

Glu Ala Leu Arg Lys Pro Thr Phe Asp Val Trp Leu Trp Glu Pro Asn
245 250 255

Glu Met Leu Ser Cys Leu Glu His Met Tyr His Asp Leu Gly Leu Val
260 265 270

Arg Asp Phe Ser Ile Asn Pro Val Thr Leu Arg Arg Trp Leu Phe Cys
275 280 285

Val His Asp Asn Tyr Arg Asn Asn Pro Phe His Asn Phe Arg His Cys
290 295 300

Phe Cys Val Ala Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser Leu
305 310 315 320

Gln Glu Lys Phe Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala Ala
325 330 335

Ile Cys His Asp Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln Ile

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          340              345              350
Asn Ala Arg Thr Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro Leu
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Glu Asn His His Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro Glu
      370              375              380

Cys Asn Ile Phe Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile Arg
385              390              395              400

Gln Gly Met Ile Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His Ala
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Glu Ile Met Asp Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr Ser
      420              425              430

Asn Glu Glu His Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys Cys
      435              440              445

Asp Ile Ser Asn Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp Val
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Asp Cys Leu Leu Glu Glu Tyr Phe Met Gln Ser Asp Arg Glu Lys Ser
465              470              475              480

Glu Gly Leu Pro Val Ala Pro Phe Met Asp Arg Asp Lys Val Thr Lys
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Ala Thr Ala Gln Ile Gly Phe Ile Lys Phe Val Leu Ile Pro Met Phe
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Glu Thr Val Thr Lys Leu Phe Pro Met Val Glu Glu Ile Met Leu Gln
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Pro Leu Trp Glu Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile Asp
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Asp Ala Met Lys Glu Leu Gln Lys Lys Thr Asp Ser Leu Thr Ser Gly
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230						235			240									
aac	tac	aga	aac	aac	ccc	ttc	cac	aac	ttc	cgg	cac	tgc	ttc	tgc	gtg	943		
Asn	Tyr	Arg	Asn	Asn	Pro	Phe	His	Asn	Phe	Arg	His	Cys	Phe	Cys	Val			
245			250			255						260						
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Ala	Gln	Met	Met	Tyr	Ser	Met	Val	Trp	Leu	Cys	Ser	Leu	Gln	Glu	Lys			
			265			270						275						
ttc	tca	caa	acg	gat	atc	ctg	atc	cta	atg	aca	gcg	gcc	atc	tgc	cac	1039		
Phe	Ser	Gln	Thr	Asp	Ile	Leu	Ile	Leu	Met	Thr	Ala	Ala	Ile	Cys	His			
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gat	ctg	gac	cat	ccc	ggc	tac	aac	aac	acg	tac	cag	atc	aat	gcc	cgc	1087		
Asp	Leu	Asp	His	Pro	Gly	Tyr	Asn	Asn	Thr	Tyr	Gln	Ile	Asn	Ala	Arg			
295						300						305						
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325			330			335						340						
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Phe	Ser	Asn	Ile	Pro	Pro	Asp	Gly	Phe	Lys	Gln	Ile	Arg	Gln	Gly	Met			
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Ile	Thr	Leu	Ile	Leu	Ala	Thr	Asp	Met	Ala	Arg	His	Ala	Glu	Ile	Met			
			360			365						370						
gat	tct	ttc	aaa	gag	aaa	atg	gag	aat	ttt	gac	tac	agc	aac	gag	gag	1327		
Asp	Ser	Phe	Lys	Glu	Lys	Met	Glu	Asn	Phe	Asp	Tyr	Ser	Asn	Glu	Glu			
375						380						385						
cac	atg	acc	ctg	ctg	aag	atg	att	ttg	ata	aaa	tgc	tgt	gat	atc	tct	1375		
His	Met	Thr	Leu	Leu	Lys	Met	Ile	Leu	Ile	Lys	Cys	Cys	Asp	Ile	Ser			
390						395			400									
aac	gag	gtc	cgt	cca	atg	gaa	gtc	gca	gag	cct	tgg	gtg	gac	tgt	tta	1423		
Asn	Glu	Val	Arg	Pro	Met	Glu	Val	Ala	Glu	Pro	Trp	Val	Asp	Cys	Leu			
405			410			415						420						
tta	gag	gaa	tat	ttt	atg	cag	agc	gac	cgt	gaga						1457		
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Thr Thr Ile Ser Leu Leu Thr Thr Asp Asp Ala Met Val Ser Ile Asp
 50 55 60

Pro Thr Met Pro Ala Asn Ser Glu Arg Thr Pro Tyr Lys Val Arg Pro
 65 70 75 80

Val Ala Ile Lys Gln Leu Ser Glu Arg Glu Glu Leu Ile Gln Ser Val
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Leu Ala Gln Val Ala Glu Gln Phe Ser Arg Ala Phe Lys Ile Asn Glu
 100 105 110

Leu Lys Ala Glu Val Ala Asn His Leu Ala Val Leu Glu Lys Arg Val
 115 120 125

Glu Leu Glu Gly Leu Lys Val Val Glu Ile Glu Lys Cys Lys Ser Asp
 130 135 140

Ile Lys Lys Met Arg Glu Glu Leu Ala Ala Arg Ser Ser Arg Thr Asn
 145 150 155 160

Cys Pro Cys Lys Tyr Ser Phe Leu Asp Asn His Lys Lys Leu Thr Pro
 165 170 175

Arg Arg Asp Val Pro Thr Tyr Pro Lys Tyr Leu Leu Ser Pro Glu Thr
 180 185 190

Ile Glu Ala Leu Arg Lys Pro Thr Phe Asp Val Trp Leu Trp Glu Pro
 195 200 205

Asn Glu Met Leu Ser Cys Leu Glu His Met Tyr His Asp Leu Gly Leu
 210 215 220

Val Arg Asp Phe Ser Ile Asn Pro Val Thr Leu Arg Arg Trp Leu Phe
 225 230 235 240

Cys Val His Asp Asn Tyr Arg Asn Asn Pro Phe His Asn Phe Arg His
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Cys Phe Cys Val Ala Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser
 260 265 270

Leu Gln Glu Lys Phe Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala

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Ile Asn Ala Arg Thr Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro		
305	310	315
Leu Glu Asn His His Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro		
	325	330
Glu Cys Asn Ile Phe Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile		
	340	345
Arg Gln Gly Met Ile Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His		
	355	360
Ala Glu Ile Met Asp Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr		
	370	375
Ser Asn Glu Glu His Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys		
385	390	395
Cys Asp Ile Ser Asn Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp		
	405	410
Val Asp Cys Leu Leu Glu Glu Tyr Phe Met Gln Ser Asp Arg		
	420	425
		430

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 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: FLAG epitope

<400> 24
 Asp Thr Lys Asp Asp Asp Asp Lys
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<210> 25
 <211> 54
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 25
 tagaccatgg actacaagga cgacgatgac aagatggacg cattcagaag cact 54

<210> 26
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 <212> DNA

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<223> Description of Artificial Sequence: primer

<400> 26

18